SEQUENCE LISTING

<110> Gendaq Limited													
	<120> Screening System												
	<130>	674538-2003											
		PCT/GB99/03730 1999-11-09											
		GB9824544.2 1998-11-09											
	<160>	16											
	<170>	PatentIn version 3.0											
	<212>	1 264 DNA Artificial Sequence											
	<222>	<pre>misc_structure (1)(264) sequence coding for a zinc finger protein</pre>											
	<400> gcagaa	1 gaga agccttttca gtgtcgaatc tgcatgcgta acttcagcga tcgtagtagt	60										
	cttacc	egec acacgaggac ccacacagge gagaageett tteagtgteg aatetgeatg	120										
	cgtaac	ittca gcaggagega taacettaeg agacacetaa ggaeceacae aggegagaag	180										
	cctttt	cagt gtcgaatctg catgcgtaac ttcaggcaag ctgatcatct tcaagagcac	240										
	ctaaag	accc acacaggcga gaag	264										
	<210><211><211><212><213>	2 88 PRT Artificial Sequence											
		<pre>ZN_FING (1)(88) protein sequence encoding a zinc-finger domain</pre>											
	<400>	2											
	Ala Gl	u Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser											

Asp Arg Ser Ser Leu Thr Arg His Thr Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Arg Gln Ala Asp His Leu Gln Glu His Leu Lys Thr His Thr Gly Glu Lys <210> 3 <211> 31 <212> PRT <213> Artificial Sequence <220> <221> VARIANT <222> (1)..(31) <223> 'X' can be any amino acid as described in the specification <400> 3 Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa His Xaa Xaa Xaa Xaa Xaa Xaa His <210> 4 <211> 31 <212> PRT <213> Artificial Sequence <220> <221> VARIANT <400> 4 Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa His Xaa Xaa Xaa Xaa Xaa Xaa Cys <210> 5 <211> 24 <212> PRT <213> Artificial Sequence

()

Ū

13 Km 4

N

##

M S

ĬÔ

C

```
<220>
<221> VARIANT
<222> (1)..(24)
<223> 'X' can be any amino acid as described in the specification
<400> 5
Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa
Leu Xaa Xaa His Xaa Xaa His
           20
<210> 6
<211> 4
<212> PRT
<213> Artificial Sequence
<220>
<221> PEPTIDE
<222> (1)..(4)
<223> linker
<400> 6
Thr Gly Glu Lys
1
<210> 7
<211> 5
<212> PRT
<213> Artificial Sequence
<220>
<221> PEPTIDE
<222> (1)..(5) <223> linker
<400> 7
Thr Gly Glu Lys Pro
<210> 8
<211> 26
<212> PRT
<213> Artificial Sequence
<220>
<221> ZN FING
<222> (1)..(26)
<223> zinc finger consensus structure
```

```
<400> 8
Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Lys Ser Asp
Leu Val Lys His Gln Arg Thr His Thr Gly
           20
<210> 9
<211> 29
<212> PRT
<213> Artificial Sequence
<220>
<221> ZN FING
<222> (1)..(29)
<223> zinc finger consensus structure
<400> 9
Pro Tyr Lys Cys Ser Glu Cys Gly Lys Ala Phe Ser Gln Lys Ser Asn
Leu Thr Arg His Gln Arg Ile His Thr Gly Glu Lys Pro
<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence
<220>
<221> PEPTIDE
<222> (1)..(6)
<223> leader peptide
<400> 10
Met Ala Glu Glu Lys Pro
<210> 11
<211> 4
<212> PRT
<213> Artificial Sequence
<220>
<221> PEPTIDE
<222> (1)..(4)
<223> smallest unit of stalling polypeptide sequence
<400> 11
```

Ç

ļ±

3

C

Ļ≟

```
Ala Ala Val Pro
    <210> 12
    <211> 24
    <212> PRT
    <213> Artificial Sequence
    <220>
    <221> PEPTIDE
    <222> (1)..(24)
    <223> linker sequence followed by the stalling polypeptide sequence
    <400> 12
    Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    Gly Gly Ser Ala Ala Val Pro
Ü
    <210> 13
Ţ
     <211> 23
tű
     <212> DNA
M
     <213> Artificial Sequence
ļi
ľU
     <220>
     <221> promoter
     <222> (1)..(23)
     <223> bacteriophage T7 RNA polymerase promoter sequence
Ü
I
    <400> 13
23
     taatacgact aactataggg aga
     <210> 14
     <211> 6
     <212> DNA
     <213> Artificial Sequence
     <220>
     <221> RBS
     <222>
           (1)..(6)
     <223> bacteriophage T7, gene 10 ribosome binding site
     <400> 14
                                                                         6
     aaggag
     <210> 15
     <211> 18
     <212> DNA
     <213> Artificial Sequence
```

```
<220>
     <221> misc_feature
     <222> (1)..(18)
     <223> DNA sequence encoding the ribosome stalling peptide sequence
     <400> 15
     atggttaaaa cagataaa
     <210> 16
     <211> 6
     <212> PRT
     <213> Artificial Sequence
     <220>
     <221> PEPTIDE
     <222> (1)..(6)
     <223> ribosome stalling peptide sequence
     <400> 16
And then the confidence of the talk
     Met Val Lys Thr Asp Lys
ļd
```

The Hall Kind dark spire green the

18

SEQUENCE LISTING

<110	> Ge	ndac	I rin	nited	1											
<120	> Sc	reer	ning	Syst	em											
<130	> p3	755														
<140	>													,		
<141	>													•		
<160	> 2															
<170> PatentIn Ver. 2.1																
<210	> 1															
<211	> 26	54														
<212	!> DN	IA														
<213> Artificial Sequence																
<220)>															
<223> Description of Artificial Sequence:Synthetic DNA																
<220																
	.> CI															
<222	?> (]		(264)	١												
<400)> 1															
gca	gaa	gag	aag	cct	ttt	cag	tgt	cga	atc	tgc	atg	cgt	aac	ttc	agc	48
Ala	Glu	Glu	Lys	Pro	Phe	Gln	Cys	Arg	Ile	Cys	Met	Arg	Asn	Phe	Ser	
1				. 5					10					15		
gat	cgt	agt	agt	ctt	acc	cgc	cac	acg	agg	acc	cac	aca	ggc	gag	aag	96
Asp	Arg	Ser	Ser	Leu	Thr	Arg	His	Thr	Arg	Thr	His	Thr	Gly	Glu	Lys	
			20					25					30			
		-	_	-		_								gat		144
Pro	Phe		Cys	Arg	Ile	Cys		Arg	Asn	Phe	Ser		Ser	Asp	Asn	
		35					40					45				
ctt	acg	aga	cac	cta	agg	acc	cac	aca	ggc	gag	aag	cct	ttt	cag	tgt	192
Leu	Thr	Arg	His	Leu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Phe	Gln	Cys	
	50					55					60					
cga	atc	tgc	atg	cgt	aac	ttc	agg	caa	gct	gat	cat	ctt	caa	gag	cac	240
Arg	Ile	Cys	Met	Arg	Asn	Phe	Arg	Gln	Ala	Asp	His	Leu	Gln	Glu	His	
65					70					75					80	

cta aag acc cac aca ggc gag aag Leu Lys Thr His Thr Gly Glu Lys 85

<210> 2

<211> 88

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:Synthetic DNA

<400> 2

Ala Glu Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser 5

Asp Arg Ser Ser Leu Thr Arg His Thr Arg Thr His Thr Gly Glu Lys 25 20

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn 40 35

Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys 60 55 50

Arg Ile Cys Met Arg Asn Phe Arg Gln Ala Asp His Leu Gln Glu His 80 75 70 65

Leu Lys Thr His Thr Gly Glu Lys 85